

SEQUENCE LISTING

<110> Obermeier, Axel  
Bieger, Boris

<120> Methods of identifying, selecting and/or characterizing compounds which  
modulate the activity of a Src family kinase

<130> 2993-1-001PCT/US

<140> PCT/EP2004/053321

<141> 2004-12-07

<150> EP 03028713.0

<151> 2003-12-12

<160> 51

<170> PatentIn version 3.1

<210> 1

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<223> Description of sequence: wt Src

<400> 1

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe

20

25

30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
 130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
 145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
 165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
 180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
 195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
 210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
 225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
 245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
 260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr  
290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu  
305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe  
340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp  
355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  
370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn  
385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val  
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val  
450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg  
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp  
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe  
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 2

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<223> Description of sequence: Src-KA

<400> 2

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Ala Thr Leu Lys Pro Gly Thr  
290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu  
305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe  
340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp  
355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  
370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn  
385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val  
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val  
450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg  
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp  
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe  
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 3

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Src-TQ

<400> 3

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
 130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
 145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
 165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
 180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
 195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
 210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
 225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
 245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
 260 265 270

Glu Val Lys<sub>275</sub> Leu Gly Gln Gly Cys<sub>280</sub> Phe Gly Glu Val Trp<sub>285</sub> Met Gly Thr  
 Trp Asn<sub>290</sub> Gly Thr Thr Arg Val<sub>295</sub> Ala Ile Lys Thr Leu<sub>300</sub> Lys Pro Gly Thr  
 Met<sub>305</sub> Ser Pro Glu Ala Phe<sub>310</sub> Leu Gln Glu Ala Gln<sub>315</sub> Val Met Lys Lys Leu<sub>320</sub>  
 Arg His Glu Lys Leu<sub>325</sub> Val Gln Leu Tyr Ala<sub>330</sub> Val Val Ser Glu Glu<sub>335</sub> Pro  
 Ile Tyr Ile Val<sub>340</sub> Gln Glu Tyr Met Ser<sub>345</sub> Lys Gly Ser Leu Leu<sub>350</sub> Asp Phe  
 Leu Lys Gly<sub>355</sub> Glu Thr Gly Lys Tyr<sub>360</sub> Leu Arg Leu Pro Gln<sub>365</sub> Leu Val Asp  
 Met Ala<sub>370</sub> Ala Gln Ile Ala Ser<sub>375</sub> Gly Met Ala Tyr Val<sub>380</sub> Glu Arg Met Asn  
 Tyr Val<sub>385</sub> His Arg Asp Leu<sub>390</sub> Arg Ala Ala Asn Ile<sub>395</sub> Leu Val Gly Glu Asn<sub>400</sub>  
 Leu Val Cys Lys Val<sub>405</sub> Ala Asp Phe Gly Leu<sub>410</sub> Ala Arg Leu Ile Glu Asp<sub>415</sub>  
 Asn Glu Tyr Thr<sub>420</sub> Ala Arg Gln Gly Ala<sub>425</sub> Lys Phe Pro Ile Lys<sub>430</sub> Trp Thr  
 Ala Pro Glu<sub>435</sub> Ala Ala Leu Tyr Gly<sub>440</sub> Arg Phe Thr Ile Lys<sub>445</sub> Ser Asp Val  
 Trp Ser<sub>450</sub> Phe Gly Ile Leu Leu<sub>455</sub> Thr Glu Leu Thr Thr<sub>460</sub> Lys Gly Arg Val  
 Pro Tyr<sub>465</sub> Pro Gly Met Val<sub>470</sub> Asn Arg Glu Val Leu<sub>475</sub> Asp Gln Val Glu Arg<sub>480</sub>  
 Gly Tyr Arg Met Pro<sub>485</sub> Cys Pro Pro Glu Cys<sub>490</sub> Pro Glu Ser Leu His Asp<sub>495</sub>  
 Leu Met Cys Gln<sub>500</sub> Cys Trp Arg Lys Glu<sub>505</sub> Pro Glu Glu Arg Pro Thr Phe  
 Glu Tyr Leu<sub>515</sub> Gln Ala Phe Leu Glu<sub>520</sub> Asp Tyr Phe Thr Ser<sub>525</sub> Thr Glu Pro



Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 4

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Src-YF

<400> 4

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
 165 170 175  
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
 180 185 190  
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
 195 200 205  
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
 210 215 220  
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
 225 230 235 240  
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
 245 250 255  
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
 260 265 270  
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
 275 280 285  
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr  
 290 295 300  
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu  
 305 310 315 320  
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
 325 330 335  
 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe  
 340 345 350  
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp  
 355 360 365  
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  
 370 375 380  
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn  
 385 390 395 400  
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp

	405		410		415
Asn	Glu	Tyr	Thr	Ala	Arg
	420			Gln	Gly
				Ala	Lys
				425	Phe
					Pro
					Ile
					Lys
					430
					Trp
					Thr
Ala	Pro	Glu	Ala	Ala	Leu
	435				Tyr
					Gly
					440
					Arg
					Phe
					Thr
					Ile
					Lys
					445
					Ser
					Asp
					Val
Trp	Ser	Phe	Gly	Ile	Leu
	450				Leu
					455
					Thr
					Glu
					Leu
					Thr
					460
					Lys
					Gly
					Arg
					Val
Pro	Tyr	Pro	Gly	Met	Val
	465				470
					Asn
					Arg
					Glu
					Val
					475
					Leu
					Asp
					Gln
					Val
					Glu
					480
					Arg
Gly	Tyr	Arg	Met	Pro	Cys
				485	Pro
					Pro
					Pro
					Glu
					Cys
					490
					Pro
					Glu
					Ser
					Leu
					His
					495
					Asp
Leu	Met	Cys	Gln	Cys	Trp
			500		Arg
					Lys
					Glu
					505
					Pro
					Glu
					Glu
					Arg
					Pro
					510
					Thr
					Phe
Glu	Tyr	Leu	Gln	Ala	Phe
					Leu
					515
					Glu
					520
					Asp
					Tyr
					Phe
					Thr
					Ser
					525
					Thr
					Glu
					Pro
Gln	Phe	Gln	Pro	Gly	Glu
	530				Asn
					535
					Leu

<210> 5

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: wt Yes

<400> 5

Met	Gly	Cys	Ile	Lys	Ser	Lys	Glu	Asn	Lys	Ser	Pro	Ala	Ile	Lys	Tyr
1				5					10					15	

Arg	Pro	Glu	Asn	Thr	Pro	Glu	Pro	Val	Ser	Thr	Ser	Val	Ser	His	Tyr
			20					25					30		

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys  
35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly  
50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val  
65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe  
85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp  
115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser  
130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe  
145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly  
165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly  
180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn  
195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile  
210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr  
225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro  
245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile  
260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe  
275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile  
 290 295 300  
 Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu  
 305 310 315 320  
 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr  
 325 330 335  
 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser  
 340 345 350  
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu  
 355 360 365  
 Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met  
 370 375 380  
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
 385 390 395 400  
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly  
 405 410 415  
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala  
 420 425 430  
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg  
 435 440 445  
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu  
 450 455 460  
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu  
 465 470 475 480  
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly  
 485 490 495  
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp  
 500 505 510  
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp  
 515 520 525  
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu

530

535

540

&lt;210&gt; 6

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Description of sequence: Yes-KA

&lt;400&gt; 6

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr  
1 5 10 15Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr  
20 25 30Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys  
35 40 45Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly  
50 55 60Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val  
65 70 75 80Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe  
85 90 95Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
100 105 110Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp  
115 120 125Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser  
130 135 140Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe  
145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly  
 165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly  
 180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn  
 195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile  
 210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr  
 225 230 235

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro  
 245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile  
 260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe  
 275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile  
 290 295 300

Ala Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu  
 305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr  
 325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser  
 340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu  
 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met  
 370 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
 385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly  
 405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala  
420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg  
435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu  
450 455 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu  
465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly  
485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp  
500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp  
515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535 540

<210> 7

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Yes-TQ

<400> 7

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr  
1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr  
20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys  
35 40 45



Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly  
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val  
 65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe  
 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp  
 115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser  
 130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe  
 145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly  
 165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly  
 180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn  
 195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile  
 210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr  
 225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro  
 245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile  
 260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe  
 275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile  
 290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu  
 305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr  
 325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe Met Ser  
 340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu  
 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met  
 370 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
 385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly  
 405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala  
 420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg  
 435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu  
 450 455 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu  
 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly  
 485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp  
 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp  
 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
 530 535 540

<210> 8

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Yes-YF

<400> 8

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr  
1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr  
20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ala Lys  
35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly  
50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val  
65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe  
85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp  
115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser  
130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe  
145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly  
165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly  
 180 185 190  
 Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn  
 195 200 205  
 Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile  
 210 215 220  
 Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr  
 225 230 235 240  
 Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro  
 245 250 255  
 Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile  
 260 265 270  
 Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe  
 275 280 285  
 Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile  
 290 295 300  
 Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu  
 305 310 315 320  
 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr  
 325 330 335  
 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser  
 340 345 350  
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu  
 355 360 365  
 Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met  
 370 375 380  
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
 385 390 395 400  
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly  
 405 410 415  
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala

420

425

430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg  
 435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu  
 450 455 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu  
 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly  
 485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp  
 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp  
 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Phe Gln Pro Gly Glu Asn Leu  
 530 535 540

&lt;210&gt; 9

&lt;211&gt; 529

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Description of sequence: wt Fgr

&lt;400&gt; 9

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys  
 1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp  
 20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala  
 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly  
 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr  
 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu  
 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly  
 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile  
 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp  
 130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser  
 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr  
 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly  
 180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr  
 195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln  
 210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro  
 225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp  
 245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly  
 260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val  
 275 280 285

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu  
 290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln  
305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe  
325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln  
340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu  
355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg  
370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp  
385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln  
405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe  
420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys  
450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro  
465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg  
485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu  
500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln  
515 520 525

Thr

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fgr-KA

<400> 10

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys  
1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp  
20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala  
35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly  
50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr  
65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu  
85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly  
100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile  
115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp  
130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser  
145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr  
165 170 175



Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly  
 180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr  
 195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln  
 210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro  
 225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp  
 245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly  
 260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val  
 275 280 285

Ala Val Ala Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu  
 290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln  
 305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe  
 325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln  
 340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu  
 355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg  
 370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp  
 385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln  
 405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe  
 420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys  
450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro  
465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg  
485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu  
500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln  
515 520 525

Thr

<210> 11

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fgr-TQ

<400> 11

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys  
1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp  
20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala  
35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly

50

55

60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr  
65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu  
85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly  
100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile  
115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp  
130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser  
145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr  
165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly  
180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr  
195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln  
210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro  
225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp  
245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly  
260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val  
275 280 285

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu  
290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln  
305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe  
325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln  
340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu  
355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg  
370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp  
385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln  
405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe  
420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys  
450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro  
465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg  
485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu  
500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln  
515 520 525

Thr

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fgr-YF

<400> 12

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys  
1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp  
20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala  
35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly  
50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr  
65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu  
85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly  
100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile  
115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp  
130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser  
145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr  
165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly

180										185					190						
Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Met	Gly	Gly	Tyr						
		195					200					205									
Tyr	Ile	Thr	Thr	Arg	Val	Gln	Phe	Asn	Ser	Val	Gln	Glu	Leu	Val	Gln						
	210					215					220										
His	Tyr	Met	Glu	Val	Asn	Asp	Gly	Leu	Cys	Asn	Leu	Leu	Ile	Ala	Pro						
225					230					235					240						
Cys	Thr	Ile	Met	Lys	Pro	Gln	Thr	Leu	Gly	Leu	Ala	Lys	Asp	Ala	Trp						
				245					250					255							
Glu	Ile	Ser	Arg	Ser	Ser	Ile	Thr	Leu	Glu	Arg	Arg	Leu	Gly	Thr	Gly						
			260					265					270								
Cys	Phe	Gly	Asp	Val	Trp	Leu	Gly	Thr	Trp	Asn	Gly	Ser	Thr	Lys	Val						
		275					280					285									
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Pro	Lys	Ala	Phe	Leu						
	290					295					300										
Glu	Glu	Ala	Gln	Val	Met	Lys	Leu	Leu	Arg	His	Asp	Lys	Leu	Val	Gln						
305					310					315					320						
Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe						
				325					330					335							
Met	Cys	His	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Asn	Pro	Glu	Gly	Gln						
			340					345					350								
Asp	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Val	Ala	Glu						
		355					360					365									
Gly	Met	Ala	Tyr	Met	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg						
	370					375					380										
Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Arg	Leu	Ala	Cys	Lys	Ile	Ala	Asp						
385					390					395					400						
Phe	Gly	Leu	Ala	Arg	Leu	Ile	Lys	Asp	Asp	Glu	Tyr	Asn	Pro	Cys	Gln						
				405					410					415							
Gly	Ser	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Phe						
			420					425					430								

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys  
450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro  
465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg  
485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu  
500 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Phe Gln Pro Gly Asp Gln  
515 520 525

Thr

<210> 13

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: wt Fyn

<400> 13

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu  
1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr  
20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro  
35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe  
50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly  
 65 70 75 80  
 Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg  
 85 90 95  
 Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu  
 100 105 110  
 Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly  
 115 120 125  
 Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile  
 130 135 140  
 Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu  
 145 150 155 160  
 Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg  
 165 170 175  
 Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp  
 180 185 190  
 Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu  
 195 200 205  
 Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu  
 210 215 220  
 Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys  
 225 230 235 240  
 Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu  
 245 250 255  
 Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln  
 260 265 270  
 Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly  
 275 280 285  
 Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly  
 290 295 300  
 Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys  
 305 310 315 320



Leu Lys His Asp Lys<sub>325</sub> Leu Val Gln Leu Tyr<sub>330</sub> Ala Val Val Ser Glu<sub>335</sub> Glu

Pro Ile Tyr Ile<sub>340</sub> Val Thr Glu Tyr<sub>345</sub> Met Asn Lys Gly Ser Leu<sub>350</sub> Leu Asp

Phe Leu Lys<sub>355</sub> Asp Gly Glu Gly Arg<sub>360</sub> Ala Leu Lys Leu Pro<sub>365</sub> Asn Leu Val

Asp Met<sub>370</sub> Ala Ala Gln Val Ala<sub>375</sub> Ala Gly Met Ala Tyr<sub>380</sub> Ile Glu Arg Met

Asn Tyr Ile His Arg Asp<sub>390</sub> Leu Arg Ser Ala Asn<sub>395</sub> Ile Leu Val Gly Asn<sub>400</sub>

Gly Leu Ile Cys Lys<sub>405</sub> Ile Ala Asp Phe Gly<sub>410</sub> Leu Ala Arg Leu Ile<sub>415</sub> Glu

Asp Asn Glu Tyr<sub>420</sub> Thr Ala Arg Gln Gly<sub>425</sub> Ala Lys Phe Pro Ile<sub>430</sub> Lys Trp

Thr Ala Pro<sub>435</sub> Glu Ala Ala Leu Tyr<sub>440</sub> Gly Arg Phe Thr Ile<sub>445</sub> Lys Ser Asp

Val Trp<sub>450</sub> Ser Phe Gly Ile Leu<sub>455</sub> Leu Thr Glu Leu Val<sub>460</sub> Thr Lys Gly Arg

Val Pro Tyr Pro Gly Met<sub>470</sub> Asn Asn Arg Glu Val<sub>475</sub> Leu Glu Gln Val Glu<sub>480</sub>

Arg Gly Tyr Arg Met<sub>485</sub> Pro Cys Pro Gln Asp<sub>490</sub> Cys Pro Ile Ser Leu<sub>495</sub> His

Glu Leu Met Ile<sub>500</sub> His Cys Trp Lys Lys<sub>505</sub> Asp Pro Glu Glu Arg<sub>510</sub> Pro Thr

Phe Glu Tyr<sub>515</sub> Leu Gln Ser Phe Leu<sub>520</sub> Glu Asp Tyr Phe Thr<sub>525</sub> Ala Thr Glu

Pro Gln Tyr Gln Pro Gly Glu<sub>535</sub> Asn Leu

<210> 14

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fyn-KA

<400> 14

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu  
1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr  
20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro  
35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe  
50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly  
65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg  
85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu  
100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly  
115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile  
130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu  
145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg  
165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp  
180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu  
 195 200 205  
 Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu  
 210 215 220  
 Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys  
 225 230 235 240  
 Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu  
 245 250 255  
 Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln  
 260 265 270  
 Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly  
 275 280 285  
 Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Ala Thr Leu Lys Pro Gly  
 290 295 300  
 Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys  
 305 310 315 320  
 Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu  
 325 330 335  
 Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp  
 340 345 350  
 Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val  
 355 360 365  
 Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met  
 370 375 380  
 Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn  
 385 390 395 400  
 Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu  
 405 410 415  
 Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp  
 420 425 430  
 Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp  
 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg  
450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu  
465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His  
485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr  
500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu  
515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 15

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fyn-TQ

<400> 15

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu  
1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr  
20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro  
35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe  
50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly

65	70							75							80		
Gly	Thr	Gly	Val	Thr 85	Leu	Phe	Val	Ala	Leu 90	Tyr	Asp	Tyr	Glu	Ala 95	Arg		
Thr	Glu	Asp	Asp 100	Leu	Ser	Phe	His	Lys 105	Gly	Glu	Lys	Phe	Gln 110	Ile	Leu		
Asn	Ser	Ser 115	Glu	Gly	Asp	Trp	Trp 120	Glu	Ala	Arg	Ser	Leu 125	Thr	Thr	Gly		
Glu	Thr 130	Gly	Tyr	Ile	Pro	Ser 135	Asn	Tyr	Val	Ala	Pro 140	Val	Asp	Ser	Ile		
Gln 145	Ala	Glu	Glu	Trp	Tyr 150	Phe	Gly	Lys	Leu	Gly 155	Arg	Lys	Asp	Ala	Glu 160		
Arg	Gln	Leu	Leu	Ser 165	Phe	Gly	Asn	Pro	Arg 170	Gly	Thr	Phe	Leu	Ile 175	Arg		
Glu	Ser	Glu	Thr 180	Thr	Lys	Gly	Ala	Tyr 185	Ser	Leu	Ser	Ile	Arg 190	Asp	Trp		
Asp	Asp	Met 195	Lys	Gly	Asp	His	Val 200	Lys	His	Tyr	Lys	Ile 205	Arg	Lys	Leu		
Asp	Asn 210	Gly	Gly	Tyr	Tyr	Ile 215	Thr	Thr	Arg	Ala	Gln 220	Phe	Glu	Thr	Leu		
Gln 225	Gln	Leu	Val	Gln	His 230	Tyr	Ser	Glu	Arg	Ala 235	Ala	Gly	Leu	Cys	Cys 240		
Arg	Leu	Val	Val	Pro 245	Cys	His	Lys	Gly	Met 250	Pro	Arg	Leu	Thr	Asp 255	Leu		
Ser	Val	Lys	Thr 260	Lys	Asp	Val	Trp	Glu 265	Ile	Pro	Arg	Glu	Ser 270	Leu	Gln		
Leu	Ile	Lys 275	Arg	Leu	Gly	Asn	Gly 280	Gln	Phe	Gly	Glu	Val 285	Trp	Met	Gly		
Thr	Trp 290	Asn	Gly	Asn	Thr	Lys 295	Val	Ala	Ile	Lys	Thr 300	Leu	Lys	Pro	Gly		
Thr 305	Met	Ser	Pro	Glu	Ser 310	Phe	Leu	Glu	Glu	Ala 315	Gln	Ile	Met	Lys	Lys 320		

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu  
325 330 335

Pro Ile Tyr Ile Val Gln Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp  
340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val  
355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met  
370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn  
385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu  
405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp  
420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp  
435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg  
450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu  
465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His  
485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr  
500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu  
515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 16

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fyn-YF

<400> 16

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu  
1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr  
20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro  
35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe  
50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly  
65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg  
85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu  
100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly  
115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile  
130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu  
145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg  
165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp  
180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu

195					200					205					
Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Glu	Thr	Leu
	210					215					220				
Gln	Gln	Leu	Val	Gln	His	Tyr	Ser	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys
225					230					235					240
Arg	Leu	Val	Val	Pro	Cys	His	Lys	Gly	Met	Pro	Arg	Leu	Thr	Asp	Leu
				245					250					255	
Ser	Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln
			260					265					270		
Leu	Ile	Lys	Arg	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly
		275					280					285			
Thr	Trp	Asn	Gly	Asn	Thr	Lys	Val	Ala	Ile	Lys	Thr	Leu	Lys	Pro	Gly
	290					295					300				
Thr	Met	Ser	Pro	Glu	Ser	Phe	Leu	Glu	Glu	Ala	Gln	Ile	Met	Lys	Lys
305					310					315					320
Leu	Lys	His	Asp	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu
				325					330					335	
Pro	Ile	Tyr	Ile	Val	Thr	Glu	Tyr	Met	Asn	Lys	Gly	Ser	Leu	Leu	Asp
			340					345					350		
Phe	Leu	Lys	Asp	Gly	Glu	Gly	Arg	Ala	Leu	Lys	Leu	Pro	Asn	Leu	Val
		355					360					365			
Asp	Met	Ala	Ala	Gln	Val	Ala	Ala	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Met
	370					375					380				
Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ser	Ala	Asn	Ile	Leu	Val	Gly	Asn
385					390					395					400
Gly	Leu	Ile	Cys	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Ile	Glu
				405					410					415	
Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp
			420					425					430		
Thr	Ala	Pro	Glu	Ala	Ala	Leu	Tyr	Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp
		435					440					445			



Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg  
450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu  
465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His  
485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr  
500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu  
515 520 525

Pro Gln Phe Gln Pro Gly Glu Asn Leu  
530 535

<210> 17

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: wt Lck

<400> 17

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn  
1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly  
20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu  
35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn  
50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu  
65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu  
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro  
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe  
115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala  
145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu  
165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr  
180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His  
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys  
210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val  
225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe  
245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val  
260 265 270

Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu  
275 280 285

Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr  
290 295 300

Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu  
305 310 315 320

Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu  
325 330 335

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met  
340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly  
370 375 380

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala  
385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr  
405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu  
420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu  
435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn  
450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg  
465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp  
485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro  
500 505

<210> 18

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lck-KA

<400> 18

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn  
1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly  
20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu  
35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn  
50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu  
65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu  
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro  
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe  
115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala  
145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu  
165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr  
180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His  
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys  
210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val  
225 230 235 240

Pro Arg Glu Thr Leu<sub>245</sub> Lys Leu Val Glu Arg<sub>250</sub> Leu Gly Ala Gly Gln Phe  
 Gly Glu Val Trp<sub>260</sub> Met Gly Tyr Tyr Asn<sub>265</sub> Gly His Thr Lys Val<sub>270</sub> Ala Val  
 Ala Ser Leu<sub>275</sub> Lys Gln Gly Ser Met<sub>280</sub> Ser Pro Asp Ala Phe<sub>285</sub> Leu Ala Glu  
 Ala Asn<sub>290</sub> Leu Met Lys Gln Leu<sub>295</sub> Gln His Gln Arg Leu<sub>300</sub> Val Arg Leu Tyr  
 Ala Val<sub>305</sub> Val Thr Gln Glu<sub>310</sub> Pro Ile Tyr Ile Ile<sub>315</sub> Thr Glu Tyr Met Glu<sub>320</sub>  
 Asn Gly Ser Leu Val<sub>325</sub> Asp Phe Leu Lys Thr<sub>330</sub> Pro Ser Gly Ile Lys<sub>335</sub> Leu  
 Thr Ile Asn Lys<sub>340</sub> Leu Leu Asp Met Ala<sub>345</sub> Ala Gln Ile Ala Glu<sub>350</sub> Gly Met  
 Ala Phe Ile<sub>355</sub> Glu Glu Arg Asn Tyr<sub>360</sub> Ile His Arg Asp Leu<sub>365</sub> Arg Ala Ala  
 Asn Ile<sub>370</sub> Leu Val Ser Asp Thr<sub>375</sub> Leu Ser Cys Lys Ile<sub>380</sub> Ala Asp Phe Gly  
 Leu Ala Arg Leu Ile Glu<sub>390</sub> Asp Asn Glu Tyr Thr<sub>395</sub> Ala Arg Glu Gly Ala<sub>400</sub>  
 Lys Phe Pro Ile Lys<sub>405</sub> Trp Thr Ala Pro Glu<sub>410</sub> Ala Ile Asn Tyr Gly<sub>415</sub> Thr  
 Phe Thr Ile Lys<sub>420</sub> Ser Asp Val Trp Ser<sub>425</sub> Phe Gly Ile Leu Leu<sub>430</sub> Thr Glu  
 Ile Val Thr<sub>435</sub> His Gly Arg Ile Pro<sub>440</sub> Tyr Pro Gly Met Thr<sub>445</sub> Asn Pro Glu  
 Val Ile<sub>450</sub> Gln Asn Leu Glu Arg<sub>455</sub> Gly Tyr Arg Met Val<sub>460</sub> Arg Pro Asp Asn  
 Cys Pro Glu Glu Leu Tyr<sub>470</sub> Gln Leu Met Arg Leu<sub>475</sub> Cys Trp Lys Glu Arg<sub>480</sub>  
 Pro Glu Asp Arg Pro<sub>485</sub> Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu<sub>495</sub> Asp

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro  
500 505

<210> 19

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lck-TQ

<400> 19

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn  
1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly  
20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu  
35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn  
50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu  
65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu  
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro  
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe  
115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala

145		150		155		160
Gly Ser Phe Ser	Leu 165	Ser Val Arg Asp	Phe 170	Asp Gln Asn Gln	Gly 175	Glu
Val Val Lys His	Tyr 180	Lys Ile Arg Asn	Leu 185	Asp Asn Gly	Gly 190	Phe Tyr
Ile Ser Pro Arg	Ile 195	Thr Phe Pro	Gly 200	Leu His Glu	Leu 205	Val Arg His
Tyr Thr Asn Ala	Ser 210	Asp Gly	Leu 215	Cys Thr Arg	Leu 220	Ser Arg Pro Cys
Gln Thr Gln Lys	Pro 225	Gln Lys Pro	Trp 230	Trp Glu	Asp 235	Glu Trp Glu Val
Pro Arg Glu Thr	Leu 245	Lys Leu Val	Glu 250	Arg Leu Gly	Ala 255	Gln Phe
Gly Glu Val Trp	Met 260	Gly Tyr Tyr	Asn 265	Gly His Thr	Lys 270	Val Ala Val
Lys Ser Leu Lys	Gln 275	Gly Ser Met	280	Ser Pro Asp	Ala 285	Phe Leu Ala Glu
Ala Asn Leu Met	Lys 290	Gln Leu Gln	His 295	Gln Arg	Leu 300	Val Arg Leu Tyr
Ala Val Val Thr	Gln 305	Glu Pro Ile	Tyr 310	Ile Ile	Gln 315	Glu Tyr Met Glu
Asn Gly Ser Leu	Val 325	Asp Phe Leu	Lys 330	Thr Pro Ser	Gly 335	Ile Lys Leu
Thr Ile Asn Lys	Leu 340	Leu Asp Met	Ala 345	Ala Gln Ile	Ala 350	Glu Gly Met
Ala Phe Ile Glu	Glu 355	Arg Asn Tyr	Ile 360	His Arg Asp	Leu 365	Arg Ala Ala
Asn Ile Leu Val	Ser 370	Asp Thr	Leu 375	Ser Cys Lys	Ile 380	Ala Asp Phe Gly
Leu Ala Arg Leu	Ile 385	Glu Asp Asn	Glu 390	Tyr Thr	Ala 395	Arg Glu Gly Ala

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr  
 405 410 415  
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu  
 420 425 430  
 Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu  
 435 440 445  
 Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn  
 450 455 460  
 Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg  
 465 470 475 480  
 Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp  
 485 490 495  
 Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro  
 500 505

<210> 20

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lck-YF

<400> 20

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn  
 1 5 10 15  
 Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly  
 20 25 30  
 Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu  
 35 40 45  
 Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn



50

55

60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu  
65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu  
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro  
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe  
115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala  
145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu  
165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr  
180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His  
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys  
210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val  
225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe  
245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val  
260 265 270

Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu  
275 280 285

Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr  
290 295 300

Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu  
305 310 315 320

Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu  
325 330 335

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met  
340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly  
370 375 380

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala  
385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr  
405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu  
420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu  
435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn  
450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg  
465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp  
485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Phe Gln Pro Gln Pro  
500 505

<210> 21

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: wt Hck

<400> 21

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu  
1 5 10 15  
Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly  
20 25 30  
Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro  
35 40 45  
Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser  
50 55 60  
His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile  
65 70 75 80  
Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu  
85 90 95  
Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu  
100 105 110  
Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro  
115 120 125  
Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe  
130 135 140  
Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
145 150 155 160  
Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys  
165 170 175  
Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp  
180 185 190  
Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr  
195 200 205  
Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His

210                      215                      220  
 Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys  
 225                      230                      235                      240  
 Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile  
                                  245                      250                      255  
 Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe  
                                  260                      265                      270  
 Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val  
                                  275                      280                      285  
 Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu  
                                  290                      295                      300  
 Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His  
 305                      310                      315                      320  
 Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala  
                                  325                      330                      335  
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln  
                                  340                      345                      350  
 Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met  
                                  355                      360                      365  
 Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
                                  370                      375                      380  
 Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly  
 385                      390                      395                      400  
 Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala  
                                  405                      410                      415  
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser  
                                  420                      425                      430  
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu  
                                  435                      440                      445  
 Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu  
                                  450                      455                      460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn  
465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg  
485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp  
500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro  
515 520 525

<210> 22

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Hck-KA

<400> 22

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu  
1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly  
20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro  
35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser  
50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile  
65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu  
85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu  
100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro  
 115 120 125  
 Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe  
 130 135 140  
 Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
 145 150 155 160  
 Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys  
 165 170 175  
 Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp  
 180 185 190  
 Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr  
 195 200 205  
 Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His  
 210 215 220  
 Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys  
 225 230 235 240  
 Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile  
 245 250 255  
 Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe  
 260 265 270  
 Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val  
 275 280 285  
 Ala Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu  
 290 295 300  
 Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His  
 305 310 315 320  
 Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala  
 325 330 335  
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln  
 340 345 350  
 Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met

355

360

365

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
 370 375 380

Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly  
 385 390 395 400

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala  
 405 410 415

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser  
 420 425 430

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu  
 435 440 445

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu  
 450 455 460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn  
 465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg  
 485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp  
 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro  
 515 520 525

&lt;210&gt; 23

&lt;211&gt; 525

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Description of sequence: Hck-TQ

&lt;400&gt; 23

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu  
 1 5 10 15  
 Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly  
 20 25 30  
 Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro  
 35 40 45  
 Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser  
 50 55 60  
 His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile  
 65 70 75 80  
 Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu  
 85 90 95  
 Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu  
 100 105 110  
 Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro  
 115 120 125  
 Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe  
 130 135 140  
 Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
 145 150 155 160  
 Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys  
 165 170 175  
 Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp  
 180 185 190  
 Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr  
 195 200 205  
 Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His  
 210 215 220  
 Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys  
 225 230 235 240  
 Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile  
 245 250 255



Pro Arg Glu Ser<sub>260</sub> Leu Lys Leu Glu Lys<sub>265</sub> Lys Leu Gly Ala Gly<sub>270</sub> Gln Phe

Gly Glu Val<sub>275</sub> Trp Met Ala Thr Tyr<sub>280</sub> Asn Lys His Thr Lys<sub>285</sub> Val Ala Val

Ala Thr<sub>290</sub> Met Lys Pro Gly Ser<sub>295</sub> Met Ser Val Glu Ala<sub>300</sub> Phe Leu Ala Glu

Ala Asn Val<sub>305</sub> Met Lys Thr<sub>310</sub> Leu Gln His Asp Lys<sub>315</sub> Leu Val Lys Leu His<sub>320</sub>

Ala Val Val<sub>325</sub> Thr Lys Glu Pro Ile Tyr Ile<sub>330</sub> Ile Gln Glu Phe Met<sub>335</sub> Ala

Lys Gly Ser<sub>340</sub> Leu Leu Asp Phe Leu Lys<sub>345</sub> Ser Asp Glu Gly Ser<sub>350</sub> Lys Gln

Pro Leu Pro<sub>355</sub> Lys Leu Ile Asp Phe<sub>360</sub> Ser Ala Gln Ile Ala<sub>365</sub> Glu Gly Met

Ala Phe<sub>370</sub> Ile Glu Gln Arg Asn<sub>375</sub> Tyr Ile His Arg Asp<sub>380</sub> Leu Arg Ala Ala

Asn Ile Leu Val<sub>385</sub> Ser Ala<sub>390</sub> Ser Leu Val Cys Lys<sub>395</sub> Ile Ala Asp Phe Gly<sub>400</sub>

Leu Ala Arg Val<sub>405</sub> Ile Glu Asp Asn Glu Tyr<sub>410</sub> Thr Ala Arg Glu Gly<sub>415</sub> Ala

Lys Phe Pro<sub>420</sub> Ile Lys Trp Thr Ala<sub>425</sub> Pro Glu Ala Ile Asn Phe<sub>430</sub> Gly Ser

Phe Thr Ile<sub>435</sub> Lys Ser Asp Val Trp<sub>440</sub> Ser Phe Gly Ile Leu<sub>445</sub> Leu Met Glu

Ile Val<sub>450</sub> Thr Tyr Gly Arg Ile<sub>455</sub> Pro Tyr Pro Gly Met<sub>460</sub> Ser Asn Pro Glu

Val Ile Arg Ala Leu<sub>465</sub> Glu Arg Gly Tyr Arg Met<sub>475</sub> Pro Arg Pro Glu Asn<sub>480</sub>

Cys Pro Glu Glu<sub>485</sub> Leu Tyr Asn Ile Met Met<sub>490</sub> Arg Cys Trp Lys Asn<sub>495</sub> Arg

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp

500

505

510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro  
 515 520 525

&lt;210&gt; 24

&lt;211&gt; 525

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Description of sequence: Hck-YF

&lt;400&gt; 24

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu  
 1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly  
 20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro  
 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser  
 50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile  
 65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu  
 85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu  
 100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro  
 115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe  
 130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
145 150 155 160

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys  
165 170 175

Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp  
180 185 190

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr  
195 200 205

Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His  
210 215 220

Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys  
225 230 235 240

Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile  
245 250 255

Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe  
260 265 270

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val  
275 280 285

Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu  
290 295 300

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His  
305 310 315 320

Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala  
325 330 335

Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln  
340 345 350

Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met  
355 360 365

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
370 375 380

Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly  
385 390 395 400

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala  
405 410 415

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser  
420 425 430

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu  
435 440 445

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu  
450 455 460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn  
465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg  
485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp  
500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Phe Gln Gln Gln Pro  
515 520 525

<210> 25

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: wt Lyn

<400> 25

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly  
1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr  
20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser  
35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln  
50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp  
65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His  
85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe  
100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu  
115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu  
130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr  
145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His  
165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly  
180 185 190

Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile  
195 200 205

Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys  
210 215 220

Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp  
225 230 235 240

Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly  
245 250 255

Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val  
260 265 270

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu  
275 280 285

Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg  
290 295 300

Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu  
305 310 315 320

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly  
325 330 335

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu  
340 345 350

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg  
355 360 365

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp  
370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu  
385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe  
405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn  
435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val  
450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys  
465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu  
485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro  
500 505 510

<210> 26

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lyn-KA

<400> 26

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly  
1 5 10 15  
Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr  
20 25 30  
Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser  
35 40 45  
Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln  
50 55 60  
Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp  
65 70 75 80  
Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His  
85 90 95  
Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe  
100 105 110  
Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu  
115 120 125  
Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu  
130 135 140  
Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr  
145 150 155 160  
Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His  
165 170 175  
Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly  
180 185 190  
Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile  
195 200 205

Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys  
 210 215 220  
 Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp  
 225 230 235 240  
 Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly  
 245 250 255  
 Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val  
 260 265 270  
 Ala Val Ala Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu  
 275 280 285  
 Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg  
 290 295 300  
 Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu  
 305 310 315 320  
 Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly  
 325 330 335  
 Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu  
 340 345 350  
 Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg  
 355 360 365  
 Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp  
 370 375 380  
 Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu  
 385 390 395 400  
 Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe  
 405 410 415  
 Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
 420 425 430  
 Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn  
 435 440 445  
 Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val



450

455

460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys  
 465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu  
 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro  
 500 505 510

&lt;210&gt; 27

&lt;211&gt; 511

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Description of sequence: Lyn-TQ

&lt;400&gt; 27

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly  
 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr  
 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser  
 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln  
 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp  
 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His  
 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe  
 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu  
115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu  
130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr  
145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His  
165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly  
180 185 190

Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile  
195 200 205

Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys  
210 215 220

Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp  
225 230 235 240

Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly  
245 250 255

Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val  
260 265 270

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu  
275 280 285

Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg  
290 295 300

Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Gln Glu  
305 310 315 320

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly  
325 330 335

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu  
340 345 350

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg  
355 360 365

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp  
370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu  
385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe  
405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn  
435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val  
450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys  
465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu  
485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro  
500 505 510

<210> 28

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lyn-YF

<400> 28

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly  
1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr

20										25					30				
Val	Arg	Asp 35	Pro	Thr	Ser	Asn	Lys 40	Gln	Gln	Arg	Pro	Val 45	Pro	Glu	Ser				
Gln	Leu 50	Leu	Pro	Gly	Gln	Arg 55	Phe	Gln	Thr	Lys	Asp 60	Pro	Glu	Glu	Gln				
Gly 65	Asp	Ile	Val	Val	Ala 70	Leu	Tyr	Pro	Tyr	Asp 75	Gly	Ile	His	Pro	Asp 80				
Asp	Leu	Ser	Phe	Lys 85	Lys	Gly	Glu	Lys	Met 90	Lys	Val	Leu	Glu	Glu	His				
Gly	Glu	Trp	Trp 100	Lys	Ala	Lys	Ser	Leu 105	Leu	Thr	Lys	Lys	Glu 110	Gly	Phe				
Ile	Pro	Ser 115	Asn	Tyr	Val	Ala	Lys 120	Leu	Asn	Thr	Leu	Glu 125	Thr	Glu	Glu				
Trp	Phe 130	Phe	Lys	Asp	Ile	Thr 135	Arg	Lys	Asp	Ala	Glu 140	Arg	Gln	Leu	Leu				
Ala 145	Pro	Gly	Asn	Ser	Ala 150	Gly	Ala	Phe	Leu	Ile 155	Arg	Glu	Ser	Glu	Thr 160				
Leu	Lys	Gly	Ser	Phe 165	Ser	Leu	Ser	Val	Arg 170	Asp	Phe	Asp	Pro	Val 175	His				
Gly	Asp	Val	Ile 180	Lys	His	Tyr	Lys	Ile 185	Arg	Ser	Leu	Asp	Asn 190	Gly	Gly				
Tyr	Tyr	Ile 195	Ser	Pro	Arg	Ile	Thr 200	Phe	Pro	Cys	Ile	Ser 205	Asp	Met	Ile				
Lys	His 210	Tyr	Gln	Lys	Gln	Ala 215	Asp	Gly	Leu	Cys	Arg 220	Arg	Leu	Glu	Lys				
Ala 225	Cys	Ile	Ser	Pro	Lys 230	Pro	Gln	Lys	Pro	Trp 235	Asp	Lys	Asp	Ala	Trp 240				
Glu	Ile	Pro	Arg	Glu 245	Ser	Ile	Lys	Leu	Val 250	Lys	Arg	Leu	Gly	Ala 255	Gly				
Gln	Phe	Gly	Glu 260	Val	Trp	Met	Gly	Tyr 265	Tyr	Asn	Asn	Ser	Thr 270	Lys	Val				

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu  
275 280 285

Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg  
290 295 300

Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu  
305 310 315 320

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly  
325 330 335

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu  
340 345 350

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg  
355 360 365

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp  
370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu  
385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe  
405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu  
420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn  
435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val  
450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys  
465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu  
485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Phe Gln Gln Gln Pro  
500 505 510

<210> 29

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: wt BLK

<400> 29

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys  
1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp  
20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr  
35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val  
50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu  
65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu  
85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe  
100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser  
115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys  
130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe  
145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His  
165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg  
180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys  
 195 200 205

Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala  
 210 215 220

Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser  
 225 230 235 240

Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp  
 245 250 255

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys  
 260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met  
 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr  
 290 295 300

Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu  
 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg  
 325 330 335

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu  
 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val  
 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile  
 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys  
 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala  
 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly  
 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu  
435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu  
450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg  
465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala  
485 490 495

Thr Glu Arg Gln Tyr Glu Leu Gln Pro  
500 505

<210> 30

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: BLK-KA

<400> 30

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys  
1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp  
20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr  
35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val  
50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu  
65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu  
85 90 95



Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe  
100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser  
115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys  
130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe  
145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His  
165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg  
180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys  
195 200 205

Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala  
210 215 220

Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser  
225 230 235 240

Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp  
245 250 255

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Ala Thr Leu Lys  
260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met  
275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr  
290 295 300

Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu  
305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg  
325 330 335

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu  
340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val  
 355 360 365  
 Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile  
 370 375 380  
 Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys  
 385 390 395 400  
 Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala  
 405 410 415  
 Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly  
 420 425 430  
 Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu  
 435 440 445  
 Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu  
 450 455 460  
 Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg  
 465 470 475 480  
 Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala  
 485 490 495  
 Thr Glu Arg Gln Tyr Glu Leu Gln Pro  
 500 505

<210> 31

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: BLK-TQ

<400> 31

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys

1	5	10	15
Glu Lys Asp	Lys Gly Gln Trp Ser	Pro Leu Lys Val Ser	Ala Gln Asp
	20	25	30
Lys Asp Ala	Pro Pro Leu Pro	Pro Leu Val Val Phe	Asn His Leu Thr
	35	40	45
Pro Pro Pro	Pro Asp Glu His	Leu Asp Glu Asp	Lys His Phe Val Val
	50	55	60
Ala Leu Tyr	Asp Tyr Thr Ala Met	Asn Asp Arg Asp	Leu Gln Met Leu
	65	70	75
Lys Gly Glu	Lys Leu Gln Val Leu	Lys Gly Thr Gly	Asp Trp Trp Leu
	85	90	95
Ala Arg Ser	Leu Val Thr Gly Arg	Glu Gly Tyr Val	Pro Ser Asn Phe
	100	105	110
Val Ala Arg	Val Glu Ser Leu Glu	Met Glu Arg Trp	Phe Phe Arg Ser
	115	120	125
Gln Gly Arg	Lys Glu Ala Glu	Arg Gln Leu Leu	Ala Pro Ile Asn Lys
	130	135	140
Ala Gly Ser	Phe Leu Ile Arg Glu	Ser Glu Thr Asn	Lys Gly Ala Phe
	145	150	155
Ser Leu Ser	Val Lys Asp Val Thr	Thr Gln Gly Glu	Leu Ile Lys His
	165	170	175
Tyr Lys Ile	Arg Cys Leu Asp Glu	Gly Gly Tyr Tyr	Ile Ser Pro Arg
	180	185	190
Ile Thr Phe	Pro Ser Leu Gln	Ala Leu Val Gln	His Tyr Ser Lys Lys
	195	200	205
Gly Asp Gly	Leu Cys Gln Arg	Leu Thr Leu Pro	Cys Val Arg Pro Ala
	210	215	220
Pro Gln Asn	Pro Trp Ala Gln	Asp Glu Trp Glu	Ile Pro Arg Gln Ser
	225	230	235
Leu Arg Leu	Val Arg Lys Leu	Gly Ser Gly Gln	Phe Gly Glu Val Trp
	245	250	255

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys  
 260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met  
 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr  
 290 295 300

Lys Glu Pro Ile Tyr Ile Val Gln Glu Tyr Met Ala Arg Gly Cys Leu  
 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg  
 325 330 335

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu  
 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val  
 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile  
 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys  
 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala  
 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly  
 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu  
 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu  
 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg  
 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala  
 485 490 495

Thr Glu Arg Gln Tyr Glu Leu Gln Pro  
 500 505

<210> 32

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: BLK-YF

<400> 32

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys  
1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp  
20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr  
35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val  
50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu  
65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu  
85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe  
100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser  
115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys  
130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe  
145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His

				165						170					175
Tyr	Lys	Ile	Arg	Cys	Leu	Asp	Glu	Gly	Gly	Tyr	Tyr	Ile	Ser	Pro	Arg
			180					185					190		
Ile	Thr	Phe	Pro	Ser	Leu	Gln	Ala	Leu	Val	Gln	His	Tyr	Ser	Lys	Lys
		195					200					205			
Gly	Asp	Gly	Leu	Cys	Gln	Arg	Leu	Thr	Leu	Pro	Cys	Val	Arg	Pro	Ala
	210					215					220				
Pro	Gln	Asn	Pro	Trp	Ala	Gln	Asp	Glu	Trp	Glu	Ile	Pro	Arg	Gln	Ser
225					230					235					240
Leu	Arg	Leu	Val	Arg	Lys	Leu	Gly	Ser	Gly	Gln	Phe	Gly	Glu	Val	Trp
				245					250					255	
Met	Gly	Tyr	Tyr	Lys	Asn	Asn	Met	Lys	Val	Ala	Ile	Lys	Thr	Leu	Lys
			260					265					270		
Glu	Gly	Thr	Met	Ser	Pro	Glu	Ala	Phe	Leu	Gly	Glu	Ala	Asn	Met	Met
		275					280					285			
Lys	Ala	Leu	Gln	His	Glu	Arg	Leu	Val	Arg	Leu	Tyr	Ala	Val	Val	Thr
	290					295					300				
Lys	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Tyr	Met	Ala	Arg	Gly	Cys	Leu
305					310					315					320
Leu	Asp	Phe	Leu	Lys	Thr	Asp	Glu	Gly	Ser	Arg	Leu	Ser	Leu	Pro	Arg
				325					330					335	
Leu	Ile	Asp	Met	Ser	Ala	Gln	Ile	Ala	Glu	Gly	Met	Ala	Tyr	Ile	Glu
			340					345					350		
Arg	Met	Asn	Ser	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val
		355					360					365			
Ser	Glu	Ala	Leu	Cys	Cys	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ile
	370					375					380				
Ile	Asp	Ser	Glu	Tyr	Thr	Ala	Gln	Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys
385					390					395					400
Trp	Thr	Ala	Pro	Glu	Ala	Ile	His	Phe	Gly	Val	Phe	Thr	Ile	Lys	Ala
				405					410					415	

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly  
420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu  
435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu  
450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg  
465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala  
485 490 495

Thr Glu Arg Gln Phe Glu Leu Gln Pro  
500 505

<210> 33

<211> 536

<212> PRT

<213> chicken

<220>

<221> misc\_feature

<223> Description of sequence: wt Yrk

<400> 33

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly  
1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro  
20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn  
35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro  
50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly  
65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr  
85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn  
100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala  
115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln  
130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg  
145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu  
165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp  
180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp  
195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln  
210 215 220

Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg  
225 230 235 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser  
245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu  
260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr  
275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr  
290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu  
305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
325 330 335



Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe  
340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp  
355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn  
370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn  
385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val  
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val  
450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg  
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp  
485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe  
500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro  
515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln  
530 535

<210> 34

<211> 536

<212> PRT

<213> chicken

<220>

<221> misc\_feature

<223> Description of sequence: Yrk-KA

<400> 34

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly  
1 5 10 15  
Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro  
20 25 30  
Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn  
35 40 45  
Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro  
50 55 60  
Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly  
65 70 75 80  
Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr  
85 90 95  
Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn  
100 105 110  
Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala  
115 120 125  
Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln  
130 135 140  
Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg  
145 150 155 160  
Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu  
165 170 175  
Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp  
180 185 190  
Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp  
195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln  
 210 215 220  
 Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg  
 225 230 235 240  
 Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser  
 245 250 255  
 Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu  
 260 265 270  
 Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr  
 275 280 285  
 Trp Asn Gly Thr Thr Lys Val Ala Val Ala Thr Leu Lys Pro Gly Thr  
 290 295 300  
 Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu  
 305 310 315 320  
 Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
 325 330 335  
 Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe  
 340 345 350  
 Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp  
 355 360 365  
 Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn  
 370 375 380  
 Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn  
 385 390 395 400  
 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
 405 410 415  
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
 420 425 430  
 Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val  
 435 440 445  
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val

450

455

460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg  
 465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp  
 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe  
 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro  
 515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln  
 530 535

&lt;210&gt; 35

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; chicken

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Description of sequence: Yrk-TQ

&lt;400&gt; 35

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly  
 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro  
 20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn  
 35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro  
 50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly  
 65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr  
 85 90 95  
 Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn  
 100 105 110  
 Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala  
 115 120 125  
 Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln  
 130 135 140  
 Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg  
 145 150 155 160  
 Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu  
 165 170 175  
 Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp  
 180 185 190  
 Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp  
 195 200 205  
 Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln  
 210 215 220  
 Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg  
 225 230 235 240  
 Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser  
 245 250 255  
 Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu  
 260 265 270  
 Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr  
 275 280 285  
 Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr  
 290 295 300  
 Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu  
 305 310 315 320  
 Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
 325 330 335

Ile Tyr Ile Val Gln Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe  
340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp  
355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn  
370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn  
385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val  
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val  
450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg  
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp  
485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe  
500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro  
515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln  
530 535

<210> 36

<211> 536

<212> PRT

<213> chicken

<220>

<221> misc\_feature

<223> Description of sequence: Yrk-YF

<400> 36

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly  
1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro  
20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn  
35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro  
50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly  
65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr  
85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn  
100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala  
115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln  
130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg  
145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu  
165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp  
180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp  
195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln  
 210 215 220  
 Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg  
 225 230 235 240  
 Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser  
 245 250 255  
 Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu  
 260 265 270  
 Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr  
 275 280 285  
 Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr  
 290 295 300  
 Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu  
 305 310 315 320  
 Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
 325 330 335  
 Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe  
 340 345 350  
 Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp  
 355 360 365  
 Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn  
 370 375 380  
 Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn  
 385 390 395 400  
 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
 405 410 415  
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
 420 425 430  
 Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val  
 435 440 445  
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val  
 450 455 460



Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg  
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp  
485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe  
500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro  
515 520 525

Gln Phe Gln Pro Gly Asp Asn Gln  
530 535

<210> 37  
<211> 536  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Src kinase (Fig. 18)

<220>  
<221> SITE  
<222> (298)  
<223> Constant amino acid K in domain SH2

<220>  
<221> SITE  
<222> (341)  
<223> Constant amino acid T in domain SH2

<220>  
<221> SITE  
<222> (530)  
<223> Constant amino acid Y in domain SH1

<400> 37  
Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
100 105 110  
Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
115 120 125  
Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
130 135 140  
Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
145 150 155 160  
Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
165 170 175  
Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
180 185 190  
Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
195 200 205  
Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
210 215 220  
Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
225 230 235 240  
Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
245 250 255  
Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
260 265 270  
Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
275 280 285  
Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr  
290 295 300  
Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu  
305 310 315 320  
Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
325 330 335  
Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe  
340 345 350  
Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp  
355 360 365  
Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  
370 375 380  
Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn  
385 390 395 400  
Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
405 410 415  
Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val  
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val  
450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg  
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp  
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe  
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 38  
<211> 543  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Yes kinase (Fig. 18)

<220>  
<221> SITE  
<222> (305)  
<223> Constant amino acid K in domain SH2

<220>  
<221> SITE  
<222> (348)  
<223> Constant amino acid T in domain SH2

<220>  
<221> SITE  
<222> (537)  
<223> Constant amino acid Y in domain SH1

<400> 38  
Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr  
1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr  
20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ala Lys  
35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly  
50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val  
65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe  
85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
100 105 110  
Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp  
115 120 125  
Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser  
130 135 140  
Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe  
145 150 155 160  
Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly  
165 170 175  
Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly  
180 185 190  
Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn  
195 200 205  
Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile  
210 215 220  
Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr  
225 230 235 240  
Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro  
245 250 255  
Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile  
260 265 270  
Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe  
275 280 285  
Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile  
290 295 300  
Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu  
305 310 315 320  
Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr  
325 330 335  
Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser  
340 345 350  
Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu  
355 360 365  
Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met  
370 375 380  
Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
385 390 395 400  
Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly  
405 410 415  
Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala  
420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg  
           435                                  440                                  445  
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu  
           450                                  455                                  460  
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu  
   465                                  470                                  475                                  480  
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly  
                                   485                                  490                                  495  
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp  
                                   500                                  505                                  510  
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp  
                                   515                                  520                                  525  
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
           530                                  535                                  540

<210> 39  
 <211> 537  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Fyn kinase (Fig. 18)

<220>  
 <221> SITE  
 <222> (299)  
 <223> Constant amino acid K in domain SH2

<220>  
 <221> SITE  
 <222> (342)  
 <223> Constant amino acid T in domain SH2

<220>  
 <221> SITE  
 <222> (531)  
 <223> Constant amino acid Y in domain SH1

<400> 39  
 Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu  
   1                                  5                                  10                                  15  
 Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr  
                                   20                                  25                                  30  
 Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro  
                                   35                                  40                                  45  
 Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe  
           50                                  55                                  60  
 Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly  
   65                                  70                                  75                                  80  
 Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg

85										90					95				
Thr	Glu	Asp	Asp	Leu	Ser	Phe	His	Lys	Gly	Glu	Lys	Phe	Gln	Ile	Leu				
			100					105					110						
Asn	Ser	Ser	Glu	Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Thr	Thr	Gly				
		115					120					125							
Glu	Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile				
	130					135					140								
Gln	Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Leu	Gly	Arg	Lys	Asp	Ala	Glu				
145					150					155					160				
Arg	Gln	Leu	Leu	Ser	Phe	Gly	Asn	Pro	Arg	Gly	Thr	Phe	Leu	Ile	Arg				
				165					170					175					
Glu	Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp				
			180					185					190						
Asp	Asp	Met	Lys	Gly	Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu				
		195					200					205							
Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Glu	Thr	Leu				
	210					215					220								
Gln	Gln	Leu	Val	Gln	His	Tyr	Ser	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys				
225					230					235					240				
Arg	Leu	Val	Val	Pro	Cys	His	Lys	Gly	Met	Pro	Arg	Leu	Thr	Asp	Leu				
				245					250					255					
Ser	Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln				
			260					265					270						
Leu	Ile	Lys	Arg	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly				
		275					280					285							
Thr	Trp	Asn	Gly	Asn	Thr	Lys	Val	Ala	Ile	Lys	Thr	Leu	Lys	Pro	Gly				
	290					295					300								
Thr	Met	Ser	Pro	Glu	Ser	Phe	Leu	Glu	Glu	Ala	Gln	Ile	Met	Lys	Lys				
305					310					315					320				
Leu	Lys	His	Asp	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu				
				325					330					335					
Pro	Ile	Tyr	Ile	Val	Thr	Glu	Tyr	Met	Asn	Lys	Gly	Ser	Leu	Leu	Asp				
			340					345					350						
Phe	Leu	Lys	Asp	Gly	Glu	Gly	Arg	Ala	Leu	Lys	Leu	Pro	Asn	Leu	Val				
		355					360					365							
Asp	Met	Ala	Ala	Gln	Val	Ala	Ala	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Met				
	370					375					380								
Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ser	Ala	Asn	Ile	Leu	Val	Gly	Asn				
385					390					395					400				
Gly	Leu	Ile	Cys	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Ile	Glu				
				405					410					415					
Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp				

	420		425		430	
Thr	Ala	Pro	Glu	Ala	Ala	Leu
	435					Tyr
						Gly
						Arg
						Phe
						Thr
						Ile
						Lys
						Ser
						Asp
Val	Trp	Ser	Phe	Gly	Ile	Leu
450						455
						Leu
						Thr
						Glu
						Leu
						Val
						460
						Thr
						Lys
						Gly
						Arg
Val	Pro	Tyr	Pro	Gly	Met	Asn
465					470	
						Asn
						Arg
						Glu
						Val
						475
						Leu
						Glu
						Gln
						Val
						480
						Glu
Arg	Gly	Tyr	Arg	Met	Pro	Cys
				485		
						Pro
						Gln
						Asp
						490
						Cys
						Pro
						Ile
						Ser
						Leu
						495
						His
Glu	Leu	Met	Ile	His	Cys	Trp
			500			
						Lys
						Lys
						505
						Asp
						Pro
						Glu
						Glu
						Arg
						510
						Pro
						Thr
Phe	Glu	Tyr	Leu	Gln	Ser	Phe
						520
						Glu
						Asp
						Tyr
						Phe
						525
						Thr
						Ala
						Thr
						Glu
Pro	Gln	Tyr	Gln	Pro	Gly	Glu
530						535
						Asn
						Leu

<210> 40  
 <211> 536  
 <212> PRT  
 <213> Chicken

<220>  
 <223> Yrk kinase (Fig. 18)

<220>  
 <221> SITE  
 <222> (298)  
 <223> Constant amino acid K in domain SH2

<220>  
 <221> SITE  
 <222> (341)  
 <223> Constant amino acid T in domain SH2

<220>  
 <221> SITE  
 <222> (530)  
 <223> Constant amino acid Y in domain SH1

<400>	40
Met	Gly
1	
	Cys
	Val
	His
	5
	Cys
	Lys
	Glu
	Lys
	10
	Ile
	Ser
	Gly
	Lys
	Gly
	15
	Gln
	Gly
Gly	Ser
	Gly
	20
	Thr
	Gly
	Thr
	25
	Pro
	Ala
	His
	25
	Pro
	Pro
	Ser
	Gln
	30
	Tyr
	Asp
	Pro
Asp	Pro
	35
	Gln
	Leu
	Ser
	Gly
	40
	Ala
	Phe
	Thr
	His
	45
	Ile
	Pro
	Asp
	Phe
	Asn
Asn	Phe
	50
	His
	Ala
	Ala
	Ala
	Val
	55
	Ser
	Pro
	Pro
	Val
	60
	Pro
	Phe
	Ser
	Gly
	Pro
Gly	Phe
	65
	Tyr
	Pro
	Cys
	70
	Asn
	Thr
	Leu
	Gln
	75
	Ala
	His
	Ser
	Ser
	Ile
	Thr
	80
	Gly

Gly Gly Val Thr Leu<sub>85</sub> Phe Ile Ala Leu Tyr<sub>90</sub> Asp Tyr Glu Ala Arg Thr  
 Glu Asp Asp Leu<sub>100</sub> Ser Phe Gln Lys Gly<sub>105</sub> Glu Lys Phe His Ile<sub>110</sub> Ile Asn  
 Asn Thr Glu<sub>115</sub> Gly Asp Trp Trp Glu<sub>120</sub> Ala Arg Ser Leu<sub>125</sub> Ser Gly Ala  
 Thr Gly<sub>130</sub> Tyr Ile Pro Ser Asn<sub>135</sub> Tyr Val Ala Pro Val<sub>140</sub> Asp Ser Ile Gln  
 Ala Glu Glu Trp Tyr Phe<sub>150</sub> Gly Lys Ile Gly Arg<sub>155</sub> Lys Asp Ala Glu Arg<sub>160</sub>  
 Gln Leu Leu Cys His<sub>165</sub> Gly Asn Cys Arg Gly<sub>170</sub> Thr Phe Leu Ile Arg<sub>175</sub> Glu  
 Ser Glu Thr Thr<sub>180</sub> Lys Gly Ala Tyr Ser<sub>185</sub> Leu Ser Ile Arg Asp<sub>190</sub> Trp Asp  
 Glu Ala Lys<sub>195</sub> Gly Asp His Val Lys<sub>200</sub> His Tyr Lys Ile Arg<sub>205</sub> Lys Leu Asp  
 Ser Gly<sub>210</sub> Gly Tyr Tyr Ile Thr<sub>215</sub> Thr Arg Ala Gln Phe<sub>220</sub> Asp Thr Ile Gln  
 Gln Leu Val Gln His Tyr<sub>230</sub> Ile Glu Arg Ala Ala<sub>235</sub> Gly Leu Cys Cys Arg<sub>240</sub>  
 Leu Ala Val Pro Cys<sub>245</sub> Pro Lys Gly Thr Pro<sub>250</sub> Lys Leu Ala Asp Leu<sub>255</sub> Ser  
 Val Lys Thr Lys<sub>260</sub> Asp Val Trp Glu Ile<sub>265</sub> Pro Arg Glu Ser Leu<sub>270</sub> Gln Leu  
 Leu Gln Lys<sub>275</sub> Leu Gly Asn Gly Gln<sub>280</sub> Phe Gly Glu Val Trp<sub>285</sub> Met Gly Thr  
 Trp Asn Gly<sub>290</sub> Thr Thr Lys Val<sub>295</sub> Ala Val Lys Thr Leu<sub>300</sub> Lys Pro Gly Thr  
 Met Ser Pro Glu Ala Phe<sub>310</sub> Leu Glu Glu Ala Gln<sub>315</sub> Ile Met Lys Arg Leu<sub>320</sub>  
 Arg His Asp Lys Leu<sub>325</sub> Val Gln Leu Tyr Ala<sub>330</sub> Val Val Ser Glu Glu<sub>335</sub> Pro  
 Ile Tyr Ile Val<sub>340</sub> Thr Glu Phe Met Ser<sub>345</sub> Gln Gly Ser Leu<sub>350</sub> Leu Asp Phe  
 Leu Lys Asp<sub>355</sub> Gly Asp Gly Arg Tyr<sub>360</sub> Leu Lys Leu Pro Gln<sub>365</sub> Leu Val Asp  
 Met Ala Ala Gln Ile Ala Ala<sub>375</sub> Gly Met Ala Tyr Ile<sub>380</sub> Glu Arg Met Asn  
 Tyr Ile His Arg Asp Leu<sub>390</sub> Arg Ala Ala Asn Ile<sub>395</sub> Leu Val Gly Asp Asn<sub>400</sub>  
 Leu Val Cys Lys Ile<sub>405</sub> Ala Asp Phe Gly Leu<sub>410</sub> Ala Arg Leu Ile Glu<sub>415</sub> Asp



Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
 420 425 430  
 Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val  
 435 440 445  
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val  
 450 455 460  
 Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg  
 465 470 475 480  
 Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp  
 485 490 495  
 Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe  
 500 505 510  
 Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro  
 515 520 525  
 Gln Tyr Gln Pro Gly Asp Asn Gln  
 530 535

<210> 41  
 <211> 529  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Fgr kinase (Fig. 18)

<220>  
 <221> SITE  
 <222> (291)  
 <223> Constant amino acid K in domain SH2

<220>  
 <221> SITE  
 <222> (334)  
 <223> Constant amino acid T in domain SH2

<220>  
 <221> SITE  
 <222> (523)  
 <223> Constant amino acid Y in domain SH1

<400> 41  
 Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys  
 1 5 10 15  
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp  
 20 25 30  
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala  
 35 40 45  
 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly  
 50 55 60  
 Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr  
 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu  
 85 90 95  
 Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly  
 100 105 110  
 Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile  
 115 120 125  
 Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp  
 130 135 140  
 Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser  
 145 150 155 160  
 Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr  
 165 170 175  
 Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly  
 180 185 190  
 Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr  
 195 200 205  
 Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln  
 210 215 220  
 His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro  
 225 230 235 240  
 Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp  
 245 250 255  
 Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly  
 260 265 270  
 Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val  
 275 280 285  
 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu  
 290 295 300  
 Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln  
 305 310 315 320  
 Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe  
 325 330 335  
 Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln  
 340 345 350  
 Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu  
 355 360 365  
 Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg  
 370 375 380  
 Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp  
 385 390 395 400  
 Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln

405										410					415				
Gly	Ser	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Phe				
			420					425					430						
Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu				
		435					440					445							
Thr	Glu	Leu	Ile	Thr	Lys	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Asn	Lys				
	450					455					460								
Arg	Glu	Val	Leu	Glu	Gln	Val	Glu	Gln	Gly	Tyr	His	Met	Pro	Cys	Pro				
465					470					475					480				
Pro	Gly	Cys	Pro	Ala	Ser	Leu	Tyr	Glu	Ala	Met	Glu	Gln	Thr	Trp	Arg				
				485					490					495					
Leu	Asp	Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu				
			500					505					510						
Glu	Asp	Tyr	Phe	Thr	Ser	Ala	Glu	Pro	Gln	Tyr	Gln	Pro	Gly	Asp	Gln				
		515					520					525							
Thr																			

<210> 42  
 <211> 525  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Hck kinase (Fig. 18)

<220>  
 <221> SITE  
 <222> (289)  
 <223> Constant amino acid K in domain SH2

<220>  
 <221> SITE  
 <222> (332)  
 <223> Constant amino acid T in domain SH2

<220>  
 <221> SITE  
 <222> (525)  
 <223> Constant amino acid Y in domain SH1

<400> 42																	
Gly	Gly	Arg	Ser	Ser	Cys	Glu	Asp	Pro	Gly	Cys	Pro	Arg	Asp	Glu	Glu		
1				5					10					15			
Arg	Ala	Pro	Arg	Met	Gly	Cys	Met	Lys	Ser	Lys	Phe	Leu	Gln	Val	Gly		
			20					25					30				
Gly	Asn	Thr	Phe	Ser	Lys	Thr	Glu	Thr	Ser	Ala	Ser	Pro	His	Cys	Pro		
		35					40					45					
Val	Tyr	Val	Pro	Asp	Pro	Thr	Ser	Thr	Ile	Lys	Pro	Gly	Pro	Asn	Ser		
	50					55					60						

His 65	Asn	Ser	Asn	Thr	Pro 70	Gly	Ile	Arg	Glu	Ala 75	Gly	Ser	Glu	Asp	Ile 80
Ile	Val	Val	Ala	Leu 85	Tyr	Asp	Tyr	Glu	Ala 90	Ile	His	His	Glu	Asp 95	Leu
Ser	Phe	Gln	Lys 100	Gly	Asp	Gln	Met	Val 105	Val	Leu	Glu	Glu	Ser 110	Gly	Glu
Trp	Trp	Lys 115	Ala	Arg	Ser	Leu	Ala 120	Thr	Arg	Lys	Glu	Gly 125	Tyr	Ile	Pro
Ser	Asn 130	Tyr	Val	Ala	Arg	Val 135	Asp	Ser	Leu	Glu	Thr 140	Glu	Glu	Trp	Phe
Phe 145	Lys	Gly	Ile	Ser	Arg 150	Lys	Asp	Ala	Glu	Arg 155	Gln	Leu	Leu	Ala	Pro 160
Gly	Asn	Met	Leu	Gly 165	Ser	Phe	Met	Ile	Arg 170	Asp	Ser	Glu	Thr	Thr 175	Lys
Gly	Ser	Tyr	Ser 180	Leu	Ser	Val	Arg	Asp 185	Tyr	Asp	Pro	Arg	Gln 190	Gly	Asp
Thr	Val 195	Lys	His	Tyr	Lys	Ile	Arg 200	Thr	Leu	Asp	Asn	Gly 205	Gly	Phe	Tyr
Ile	Ser 210	Pro	Arg	Ser	Thr	Phe 215	Ser	Thr	Leu	Gln	Glu 220	Leu	Val	Asp	His
Tyr 225	Lys	Lys	Gly	Asn	Asp 230	Gly	Leu	Cys	Gln	Lys 235	Leu	Ser	Val	Pro	Cys 240
Met	Ser	Ser	Lys	Pro 245	Gln	Lys	Pro	Trp	Glu 250	Lys	Asp	Ala	Trp	Glu 255	Ile
Pro	Arg	Glu	Ser 260	Leu	Lys	Leu	Glu	Lys 265	Lys	Leu	Gly	Ala	Gly 270	Gln	Phe
Gly	Glu	Val 275	Trp	Met	Ala	Thr	Tyr 280	Asn	Lys	His	Thr	Lys 285	Val	Ala	Val
Lys	Thr 290	Met	Lys	Pro	Gly	Ser 295	Met	Ser	Val	Glu	Ala 300	Phe	Leu	Ala	Glu
Ala 305	Asn	Val	Met	Lys	Thr 310	Leu	Gln	His	Asp	Lys 315	Leu	Val	Lys	Leu	His 320
Ala	Val	Val	Thr	Lys 325	Glu	Pro	Ile	Tyr	Ile 330	Ile	Thr	Glu	Phe	Met 335	Ala
Lys	Gly	Ser	Leu 340	Leu	Asp	Phe	Leu	Lys 345	Ser	Asp	Glu	Gly	Ser 350	Lys	Gln
Pro	Leu	Pro 355	Lys	Leu	Ile	Asp	Phe 360	Ser	Ala	Gln	Ile	Ala 365	Glu	Gly	Met
Ala	Phe 370	Ile	Glu	Gln	Arg	Asn 375	Tyr	Ile	His	Arg	Asp 380	Leu	Arg	Ala	Ala
Asn 385	Ile	Leu	Val	Ser	Ala 390	Ser	Leu	Val	Cys	Lys 395	Ile	Ala	Asp	Phe	Gly 400



65	70					75					80				
Asp	Leu	Ser	Phe	Lys <sub>85</sub>	Lys	Gly	Glu	Lys	Met <sub>90</sub>	Lys	Val	Leu	Glu	Glu <sub>95</sub>	His
Gly	Glu	Trp	Trp <sub>100</sub>	Lys	Ala	Lys	Ser	Leu <sub>105</sub>	Leu	Thr	Lys	Lys	Glu <sub>110</sub>	Gly	Phe
Ile	Pro	Ser <sub>115</sub>	Asn	Tyr	Val	Ala	Lys <sub>120</sub>	Leu	Asn	Thr	Leu	Glu <sub>125</sub>	Thr	Glu	Glu
Trp	Phe <sub>130</sub>	Phe	Lys	Asp	Ile	Thr <sub>135</sub>	Arg	Lys	Asp	Ala	Glu <sub>140</sub>	Arg	Gln	Leu	Leu
Ala <sub>145</sub>	Pro	Gly	Asn	Ser	Ala <sub>150</sub>	Gly	Ala	Phe	Leu	Ile <sub>155</sub>	Arg	Glu	Ser	Glu	Thr <sub>160</sub>
Leu	Lys	Gly	Ser	Phe <sub>165</sub>	Ser	Leu	Ser	Val	Arg <sub>170</sub>	Asp	Phe	Asp	Pro	Val <sub>175</sub>	His
Gly	Asp	Val	Ile <sub>180</sub>	Lys	His	Tyr	Lys	Ile <sub>185</sub>	Arg	Ser	Leu	Asp	Asn <sub>190</sub>	Gly	Gly
Tyr	Tyr	Ile <sub>195</sub>	Ser	Pro	Arg	Ile	Thr <sub>200</sub>	Phe	Pro	Cys	Ile	Ser <sub>205</sub>	Asp	Met	Ile
Lys	His <sub>210</sub>	Tyr	Gln	Lys	Gln	Ala <sub>215</sub>	Asp	Gly	Leu	Cys	Arg <sub>220</sub>	Arg	Leu	Glu	Lys
Ala <sub>225</sub>	Cys	Ile	Ser	Pro	Lys <sub>230</sub>	Pro	Gln	Lys	Pro	Trp <sub>235</sub>	Asp	Lys	Asp	Ala	Trp <sub>240</sub>
Glu	Ile	Pro	Arg	Glu <sub>245</sub>	Ser	Ile	Lys	Leu	Val <sub>250</sub>	Lys	Arg	Leu	Gly	Ala <sub>255</sub>	Gly
Gln	Phe	Gly	Glu <sub>260</sub>	Val	Trp	Met	Gly	Tyr <sub>265</sub>	Tyr	Asn	Asn	Ser	Thr <sub>270</sub>	Lys	Val
Ala	Val	Lys <sub>275</sub>	Thr	Leu	Lys	Pro	Gly <sub>280</sub>	Thr	Met	Ser	Val	Gln <sub>285</sub>	Ala	Phe	Leu
Glu	Glu <sub>290</sub>	Ala	Asn	Leu	Met	Lys <sub>295</sub>	Thr	Leu	Gln	His	Asp <sub>300</sub>	Lys	Leu	Val	Arg
Leu	Tyr	Ala	Val	Val	Thr <sub>310</sub>	Arg	Glu	Glu	Pro	Ile <sub>315</sub>	Tyr	Ile	Ile	Thr	Glu <sub>320</sub>
Tyr	Met	Ala	Lys	Gly <sub>325</sub>	Ser	Leu	Leu	Asp	Phe <sub>330</sub>	Leu	Lys	Ser	Asp	Glu <sub>335</sub>	Gly
Gly	Lys	Val	Leu <sub>340</sub>	Leu	Pro	Lys	Leu	Ile <sub>345</sub>	Asp	Phe	Ser	Ala	Gln <sub>350</sub>	Ile	Ala
Glu	Gly	Met <sub>355</sub>	Ala	Tyr	Ile	Glu	Arg <sub>360</sub>	Lys	Asn	Tyr	Ile	His <sub>365</sub>	Arg	Asp	Leu
Arg	Ala <sub>370</sub>	Ala	Asn	Val	Leu	Val <sub>375</sub>	Ser	Glu	Ser	Leu	Met <sub>380</sub>	Cys	Lys	Ile	Ala
Asp <sub>385</sub>	Phe	Gly	Leu	Ala	Arg <sub>390</sub>	Val	Ile	Glu	Asp	Asn <sub>395</sub>	Glu	Tyr	Thr	Ala	Arg <sub>400</sub>
Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn

	405		410		415
Phe Gly Cys	Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu				
	420		425		430
Leu Tyr Glu	Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr				
	435		440		445
Asn Ala Asp	Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg				
	450		455		460
Val Glu Asn Cys	Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp				
	465		470		475
Lys Glu Lys Ala	Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val				
	485		490		495
Leu Asp Asp	Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro				
	500		505		510

<210> 44  
 <211> 509  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Lck kinase (Fig. 18)

<220>  
 <221> SITE  
 <222> (273)  
 <223> Constant amino acid K in domain SH2

<220>  
 <221> SITE  
 <222> (316)  
 <223> Constant amino acid T in domain SH2

<220>  
 <221> SITE  
 <222> (505)  
 <223> Constant amino acid Y in domain SH1

<400> 44	
Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn	
1 5 10 15	
Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly	
20 25 30	
Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu	
35 40 45	
Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn	
50 55 60	
Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu	
65 70 75 80	
Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu	
85 90 95	

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro  
 100 105 110  
 Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe  
 115 120 125  
 Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro  
 130 135 140  
 Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala  
 145 150 155 160  
 Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu  
 165 170 175  
 Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr  
 180 185 190  
 Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His  
 195 200 205  
 Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys  
 210 215 220  
 Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val  
 225 230 235 240  
 Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe  
 245 250 255  
 Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val  
 260 265 270  
 Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu  
 275 280 285  
 Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr  
 290 295 300  
 Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu  
 305 310 315 320  
 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu  
 325 330 335  
 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met  
 340 345 350  
 Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala  
 355 360 365  
 Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly  
 370 375 380  
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala  
 385 390 395 400  
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr  
 405 410 415  
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu  
 420 425 430



Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu  
 435 440 445  
 Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn  
 450 455 460  
 Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg  
 465 470 475 480  
 Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp  
 485 490 495  
 Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro  
 500 505

<210> 45  
 <211> 505  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Blk kinase (Fig. 18)

<220>  
 <221> SITE  
 <222> (269)  
 <223> Constant amino acid K in domain SH2

<220>  
 <221> SITE  
 <222> (312)  
 <223> Constant amino acid T in domain SH2

<220>  
 <221> SITE  
 <222> (501)  
 <223> Constant amino acid Y in domain SH1

<400> 45  
 Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys  
 1 5 10 15  
 Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp  
 20 25 30  
 Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr  
 35 40 45  
 Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val  
 50 55 60  
 Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu  
 65 70 75 80  
 Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu  
 85 90 95  
 Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe  
 100 105 110  
 Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser  
 115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys  
 130 135 140  
 Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe  
 145 150 155 160  
 Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His  
 165 170 175  
 Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg  
 180 185 190  
 Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys  
 195 200 205  
 Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala  
 210 215 220  
 Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser  
 225 230 235 240  
 Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp  
 245 250 255  
 Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys  
 260 265 270  
 Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met  
 275 280 285  
 Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr  
 290 295 300  
 Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu  
 305 310 315 320  
 Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg  
 325 330 335  
 Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu  
 340 345 350  
 Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val  
 355 360 365  
 Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile  
 370 375 380  
 Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys  
 385 390 395 400  
 Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala  
 405 410 415  
 Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly  
 420 425 430  
 Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu  
 435 440 445  
 Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu  
 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg  
 465 470 475 480  
 Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala  
 485 490 495  
 Thr Glu Arg Gln Tyr Glu Leu Gln Pro  
 500 505

<210> 46  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Oligonucleotide (sense) used for the generation of  
 Src-K298A (page 35 of description)

<400> 46  
 ccagggtggc catcgccacc ctgaagcctg gcac 34

<210> 47  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Oligonucleotide (antisense) used for the  
 generation of Src-K298A (page 35 of description)

<400> 47  
 gtgccaggct tcagggtggc gatggccacc ctgg 34

<210> 48  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Oligonucleotide (sense) used for the generation of  
 Src-T341Q (page 35 of description)

<400> 48  
 ccatttacat cgtccaggag tacatgagca ag 32

<210> 49  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Oligonucleotide (antisense) used for the  
 generation of Src-T341Q (page 35 of description)

<400> 49  
cttgctcatg tactcctgga cgatgtaaat gg 32

<210> 50  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide (sense) used for the generation of  
Src-Y530F (page 35 of description)

<400> 50  
ccaccgagcc ccagttccag cccggggag 29

<210> 51  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide (antisense) used for the  
generation of Src-Y530F (page 35 of description)

<400> 51  
ctccccgggc tggaactggg gctcgggtg 29